RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/547,660_

Source: _PY//o_

Date Processed by STIC: _9/13/05_

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    RAW SEQUENCE LISTING                        DATE: 09/13/2005
    PATENT APPLICATION:  US/10/547,660          TIME: 10:16:41

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    Output Set: N:\CRF4\09132005\J547660.raw
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      3 <110> APPLICANT: Hofvander, Per
      4         Andersson, Mariette
      6 <120> TITLE OF INVENTION: ENHANCED AMYLOSE PRODUCTION IN PLANTS
      8 <130> FILE REFERENCE: 12810-00125-US
C-->  10 <140> CURRENT APPLICATION NUMBER: US/10/547,660
C-->  10 <141> CURRENT FILING DATE: 2005-09-01
     10 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/002096
     11 <151> PRIOR FILING DATE: 2004-03-03
     13 <150> PRIOR APPLICATION NUMBER: EP03005181.7
     14 <151> PRIOR FILING DATE: 2003-03-07
     16 <160> NUMBER OF SEQ ID NOS: 38
     18 <170> SOFTWARE: PatentIn version 3.3
     20 <210> SEQ ID NO: 1
     21 <211> LENGTH: 2084
     22 <212> TYPE: DNA
     23 <213> ORGANISM: Solanum tuberosum
     25 <220> FEATURE:
     26 <221> NAME/KEY: CDS
     27 <222> LOCATION: (302)..(1696)
     29 <400> SEQUENCE: 1
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     32 tttttttgttt gttgatattc tcttgaaaat tgttcagtga agagttgatc aaagctaaga 120
     34 cacaggggct gcggccattt tttcaccgga atcttcttct ttattttccg gtgaaagttt 180
     36 gaacgcacac cgttatttct agacagtaga caatgtcaag tgaaaaacat cacaagtttt 240
     38 tgaagatttg taattaatta gttgagattt ttaatttgga ggaaagagaa aaacagagaa 300
     40 g atg ata ggg cgg gtg ggc ttg ttg ttg gta ttg ttg ata gca acg acg 349
     41   Met Ile Gly Arg Val Gly Leu Leu Leu Val Leu Leu Ile Ala Thr Thr
     42    1               5                  10                  15
     44 gtg act att ggg gct gaa acg acg acg tta aaa ggg gta aac aga aat     397
     45 Val Thr Ile Gly Ala Glu Thr Thr Thr Leu Lys Gly Val Asn Arg Asn
     46             20                  25                  30
     48 gcg tat gcg act atg atg tat atg gga act ccg aga gac tac gag ttc     445
     49 Ala Tyr Ala Thr Met Met Tyr Met Gly Thr Pro Arg Asp Tyr Glu Phe
     50         35                  40                  45
     52 tac gtg gcg act cga gta atg ctc cga tca ctt acc cgg cta gga gtt     493
     53 Tyr Val Ala Thr Arg Val Met Leu Arg Ser Leu Thr Arg Leu Gly Val
     54     50                  55                  60
     56 gaa gcc gat ctc gtc gtt att gct tca ctt gac gtt cct ctt cgc tgg     541
     57 Glu Ala Asp Leu Val Val Ile Ala Ser Leu Asp Val Pro Leu Arg Trp
     58 65                  70                  75                  80
     60 gtt caa act cta gaa cag gaa gat ggt gct aag gtg gtg aga gtt aaa     589
     61 Val Gln Thr Leu Glu Gln Glu Asp Gly Ala Lys Val Val Arg Val Lys
     62                 85                  90                  95
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64 aat ctg aac aat ccg tat tgt atc aac cct aat tgg aga ttc aag ctc   637
65 Asn Leu Asn Asn Pro Tyr Cys Ile Asn Pro Asn Trp Arg Phe Lys Leu
66             100                 105                 110
68 aca ctg aac aaa ctt tat gcg tgg agc ctc gta aat tat gac agg gtt   685
69 Thr Leu Asn Lys Leu Tyr Ala Trp Ser Leu Val Asn Tyr Asp Arg Val
70             115                 120                 125
72 gtc atg ctt gat gct gac aac ctt ttc ctc cag aaa act gat gaa ctg   733
73 Val Met Leu Asp Ala Asp Asn Leu Phe Leu Gln Lys Thr Asp Glu Leu
74         130                 135                 140
76 ttc caa tgt ggc cag ttt tgt gct gtc ttc att aat ccc tgc atc ttc   781
77 Phe Gln Cys Gly Gln Phe Cys Ala Val Phe Ile Asn Pro Cys Ile Phe
78 145                 150                 155                 160
80 cac act ggt ctc ttt gta ttg cag cca tca aaa aag gtg ttc aat gac   829
81 His Thr Gly Leu Phe Val Leu Gln Pro Ser Lys Lys Val Phe Asn Asp
82             165                 170                 175
84 atg atc cat gag ata gag att ggg agg gaa aat caa gac ggt gca gac   877
85 Met Ile His Glu Ile Glu Ile Gly Arg Glu Asn Gln Asp Gly Ala Asp
86             180                 185                 190
88 caa ggt ttt att gga ggc cac ttc cca gat tta ctt gat cgg cca atg   925
89 Gln Gly Phe Ile Gly Gly His Phe Pro Asp Leu Leu Asp Arg Pro Met
90             195                 200                 205
92 ttc cac cct cct ctt aat ggt acc cag ctc cag gga agt tac agg ctt   973
93 Phe His Pro Pro Leu Asn Gly Thr Gln Leu Gln Gly Ser Tyr Arg Leu
94         210                 215                 220
96 cct cta gga tac caa atg gac gcc tct tat tat tat ctc aaa ctc cat   1021
97 Pro Leu Gly Tyr Gln Met Asp Ala Ser Tyr Tyr Tyr Leu Lys Leu His
98 225                 230                 235                 240
100 tgg tcg gta cct tgt gga cct aat agt gtc att aca ttt cct ggt gct   1069
101 Trp Ser Val Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly Ala
102                 245                 250                 255
104 cca tgg tta aaa cca tgg tat tgg tgg tca tgg cct gtc tta ccc ttg   1117
105 Pro Trp Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro Leu
106             260                 265                 270
108 ggc atc cag tgg cat gaa cag cga cgt cta act gtt ggg tat ggt gct   1165
109 Gly Ile Gln Trp His Glu Gln Arg Arg Leu Thr Val Gly Tyr Gly Ala
110             275                 280                 285
112 gag atg ata gca gtg ttg atc caa tct ata ttt tac cta gga ata att   1213
113 Glu Met Ile Ala Val Leu Ile Gln Ser Ile Phe Tyr Leu Gly Ile Ile
114         290                 295                 300
116 gca gtg aca cgc cta gca cgc cca aat tta tca aag ttg tgc tat cgc   1261
117 Ala Val Thr Arg Leu Ala Arg Pro Asn Leu Ser Lys Leu Cys Tyr Arg
118 305                 310                 315                 320
120 cat gat gat agc aag agt gcc ttc tta cta cga act ggc ctt aaa ttg   1309
121 His Asp Asp Ser Lys Ser Ala Phe Leu Leu Arg Thr Gly Leu Lys Leu
122                 325                 330                 335
124 att gct ata tgg tcc att ctt gct gcc tac aca gtt cct tat ttc gtg   1357
125 Ile Ala Ile Trp Ser Ile Leu Ala Ala Tyr Thr Val Pro Tyr Phe Val
126             340                 345                 350
128 att cct tgt aca gtt cat cca cta gtt ggc tgg agt ctc tac tta ctc   1405
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129 Ile Pro Cys Thr Val His Pro Leu Val Gly Trp Ser Leu Tyr Leu Leu
130         355             360             365
132 ggc tct ttt tca cta tcc tgt ata aca gtg aat gca ttt ctt ttg ccg   1453
133 Gly Ser Phe Ser Leu Ser Cys Ile Thr Val Asn Ala Phe Leu Leu Pro
134         370             375             380
136 atg cta cct gtt tta gtc cca tgg att ggg atc ctt ggg gcc ctt ttg   1501
137 Met Leu Pro Val Leu Val Pro Trp Ile Gly Ile Leu Gly Ala Leu Leu
138 385             390             395             400
140 gtg atg gct tac cct tgg tac aac gac ggt gtt gta aga gca atg gct   1549
141 Val Met Ala Tyr Pro Trp Tyr Asn Asp Gly Val Val Arg Ala Met Ala
142             405             410             415
144 gta ttt aca tac gcc ttc tgt gct tct cca gca tta tgg atg gca ttg   1597
145 Val Phe Thr Tyr Ala Phe Cys Ala Ser Pro Ala Leu Trp Met Ala Leu
146             420             425             430
148 gtt aaa atc aag tgt tct ctt cat gtt tca ctt gag agg gaa gga ttc   1645
149 Val Lys Ile Lys Cys Ser Leu His Val Ser Leu Glu Arg Glu Gly Phe
150         435             440             445
152 ttg ccc aag ata agt gaa tct aca gca cct gct ggt tct aac aaa ctg   1693
153 Leu Pro Lys Ile Ser Glu Ser Thr Ala Pro Ala Gly Ser Asn Lys Leu
154         450             455             460
156 tat tgaaagttga aaagttaaag gaatcaacag gagaactaat gcttcagaaa         1746
157 Tyr
158 465
160 catctccaaa cgttttgctt aggagacttg gagtctgctt gtgctatcct agctagttgc 1806
162 ttcagtctgt gctcttaatt agaatggaat tctgtgagtg ggtttagaat tgggaggatg 1866
164 ttttgtgttg tacatggact atctctggtc tcttgaatgc tactccagga aaaagattgt 1926
166 ttctcactta attttttctg ttactaaatt gtatgtggaa taggttcttt aaaatttatt 1986
168 catggattta tgttatgtat gctaacagtg taaatattaa gtcctggtga aataagtaat 2046
170 tccttattca tacaaaaaaa aaaaaaaaa aaaaaaaa                          2084
173 <210> SEQ ID NO: 2
174 <211> LENGTH: 465
175 <212> TYPE: PRT
176 <213> ORGANISM: Solanum tuberosum
178 <400> SEQUENCE: 2
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182 Val Thr Ile Gly Ala Glu Thr Thr Thr Leu Lys Gly Val Asn Arg Asn
183             20              25              30
185 Ala Tyr Ala Thr Met Met Tyr Met Gly Thr Pro Arg Asp Tyr Glu Phe
186         35              40              45
188 Tyr Val Ala Thr Arg Val Met Leu Arg Ser Leu Thr Arg Leu Gly Val
189     50              55              60
191 Glu Ala Asp Leu Val Val Ile Ala Ser Leu Asp Val Pro Leu Arg Trp
192 65              70              75              80
194 Val Gln Thr Leu Glu Gln Glu Asp Gly Ala Lys Val Val Arg Val Lys
195             85              90              95
197 Asn Leu Asn Asn Pro Tyr Cys Ile Asn Pro Asn Trp Arg Phe Lys Leu
198         100             105             110
200 Thr Leu Asn Lys Leu Tyr Ala Trp Ser Leu Val Asn Tyr Asp Arg Val
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201          115                120                125
203 Val Met Leu Asp Ala Asp Asn Leu Phe Leu Gln Lys Thr Asp Glu Leu
204     130                135                140
206 Phe Gln Cys Gly Gln Phe Cys Ala Val Phe Ile Asn Pro Cys Ile Phe
207 145              150                155                160
209 His Thr Gly Leu Phe Val Leu Gln Pro Ser Lys Lys Val Phe Asn Asp
210              165                170                175
212 Met Ile His Glu Ile Glu Ile Gly Arg Glu Asn Gln Asp Gly Ala Asp
213          180                185                190
215 Gln Gly Phe Ile Gly Gly His Phe Pro Asp Leu Leu Asp Arg Pro Met
216          195                200                205
218 Phe His Pro Pro Leu Asn Gly Thr Gln Leu Gln Gly Ser Tyr Arg Leu
219     210                215                220
221 Pro Leu Gly Tyr Gln Met Asp Ala Ser Tyr Tyr Tyr Leu Lys Leu His
222 225                230                235                240
224 Trp Ser Val Pro Cys Gly Pro Asn Ser Val Ile Thr Phe Pro Gly Ala
225              245                250                255
227 Pro Trp Leu Lys Pro Trp Tyr Trp Trp Ser Trp Pro Val Leu Pro Leu
228          260                265                270
230 Gly Ile Gln Trp His Glu Gln Arg Arg Leu Thr Val Gly Tyr Gly Ala
231          275                280                285
233 Glu Met Ile Ala Val Leu Ile Gln Ser Ile Phe Tyr Leu Gly Ile Ile
234     290                295                300
236 Ala Val Thr Arg Leu Ala Arg Pro Asn Leu Ser Lys Leu Cys Tyr Arg
237 305              310                315                320
239 His Asp Asp Ser Lys Ser Ala Phe Leu Leu Arg Thr Gly Leu Lys Leu
240              325                330                335
242 Ile Ala Ile Trp Ser Ile Leu Ala Ala Tyr Thr Val Pro Tyr Phe Val
243          340                345                350
245 Ile Pro Cys Thr Val His Pro Leu Val Gly Trp Ser Leu Tyr Leu Leu
246          355                360                365
248 Gly Ser Phe Ser Leu Ser Cys Ile Thr Val Asn Ala Phe Leu Leu Pro
249     370                375                380
251 Met Leu Pro Val Leu Val Pro Trp Ile Gly Ile Leu Gly Ala Leu Leu
252 385              390                395                400
254 Val Met Ala Tyr Pro Trp Tyr Asn Asp Gly Val Val Arg Ala Met Ala
255              405                410                415
257 Val Phe Thr Tyr Ala Phe Cys Ala Ser Pro Ala Leu Trp Met Ala Leu
258          420                425                430
260 Val Lys Ile Lys Cys Ser Leu His Val Ser Leu Glu Arg Glu Gly Phe
261          435                440                445
263 Leu Pro Lys Ile Ser Glu Ser Thr Ala Pro Ala Gly Ser Asn Lys Leu
264     450                455                460
266 Tyr
267 465
271 <210> SEQ ID NO: 3
272 <211> LENGTH: 2230
273 <212> TYPE: DNA
274 <213> ORGANISM: Solanum tuberosum
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RAW SEQUENCE LISTING   DATE: 09/13/2005
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276 <220> FEATURE:
277 <221> NAME/KEY: CDS
278 <222> LOCATION: (143)..(2086)
280 <400> SEQUENCE: 3
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285 acttgaaaaa ggaaagccca ga atg aga gga agt tta gct ggt gga cca cct 172
286                         Met Arg Gly Ser Leu Ala Gly Gly Pro Pro
287                          1                 5                  10
289 agt cct att gaa cct aga cag agg ctt tct gta ttc act gag gaa aca 220
290 Ser Pro Ile Glu Pro Arg Gln Arg Leu Ser Val Phe Thr Glu Glu Thr
291              15              20                  25
293 agc aaa aga agg ttc ttg aga agt aaa gtt ttc aga gat ggg gag aga 268
294 Ser Lys Arg Arg Phe Leu Arg Ser Lys Val Phe Arg Asp Gly Glu Arg
295          30              35                  40
297 gct ctt cat agt ccc acc aaa aac agg aat ttt acc tgc aag ttc cca 316
298 Ala Leu His Ser Pro Thr Lys Asn Arg Asn Phe Thr Cys Lys Phe Pro
299          45              50                  55
301 act gtg aag ctt ata ttg ggt gtt att gct ctg gtt gca att tgg tca 364
302 Thr Val Lys Leu Ile Leu Gly Val Ile Ala Leu Val Ala Ile Trp Ser
303      60              65                  70
305 ctc tgg cat tct cca gca att tat aac acg gaa tac ata tct agt tca 412
306 Leu Trp His Ser Pro Ala Ile Tyr Asn Thr Glu Tyr Ile Ser Ser Ser
307 75              80                  85                  90
309 ggc tct cgg gct gct ttg atg cac aga gag tta agt ggt cat tct tca 460
310 Gly Ser Arg Ala Ala Leu Met His Arg Glu Leu Ser Gly His Ser Ser
311              95              100                 105
313 gct gat caa cgt tat aca tca ctt tta gat att gac tgg gac caa att 508
314 Ala Asp Gln Arg Tyr Thr Ser Leu Leu Asp Ile Asp Trp Asp Gln Ile
315              110             115                 120
317 tcc caa gtt att gag aaa ctg gcc gat agg cat gag tat cag ggc gta 556
318 Ser Gln Val Ile Glu Lys Leu Ala Asp Arg His Glu Tyr Gln Gly Val
319          125             130                 135
321 ggg ata tta aac ttc aat gac agt gaa att gat cag ttg aag gag tta 604
322 Gly Ile Leu Asn Phe Asn Asp Ser Glu Ile Asp Gln Leu Lys Glu Leu
323      140             145                 150
325 cta ccg gac gct gag cat gta atc ttg aac ctg gat cac gtc ccg aat 652
326 Leu Pro Asp Ala Glu His Val Ile Leu Asn Leu Asp His Val Pro Asn
327 155             160                 165                 170
329 aat ata aca tgg gaa aca ata tat cct gaa tgg ata gat gaa gaa gaa 700
330 Asn Ile Thr Trp Glu Thr Ile Tyr Pro Glu Trp Ile Asp Glu Glu Glu
331              175             180                 185
333 gaa ttt gag gtc ccc act tgt cct tct ctg ccc aaa att cag ttt ccg 748
334 Glu Phe Glu Val Pro Thr Cys Pro Ser Leu Pro Lys Ile Gln Phe Pro
335          190             195                 200
337 ggt aaa cca agg att gat ctc ata gtt gta aag ctt cca tgc aag aag 796
338 Gly Lys Pro Arg Ile Asp Leu Ile Val Val Lys Leu Pro Cys Lys Lys
339          205             210                 215
341 tct aag gac tgg tat aga gat gta gct cgt ttt cac ttg cag ctg gca 844
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VERIFICATION SUMMARY   DATE: 09/13/2005
PATENT APPLICATION: **US/10/547,660**   TIME: 10:16:42

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